What is claimed is:

1. A method for screening for transcription factor modulators, the method comprising:

forming a plurality of test samples by contacting samples of cells with different agents; and

for each test sample, identifying which of a plurality of different activated transcription factors are present by

taking a library of double stranded transcription factor probes, the transcription factor probes each comprising a recognition sequence capable of binding to an activated transcription factor, the recognition sequence varying within the library for binding to different activated transcription factors,

contacting the different test sample with the library of double stranded DNA probes under conditions where DNA probe - transcription factor complexes are formed between the DNA probes and activated transcription factors present in the test samples,

isolating the transcription factor probes from the transcription factor probe - transcription factor complexes formed, and

identifying which transcription factor probes in the library formed complexes by taking an array of immobilized hybridization probes capable of hybridizing to at least one of the strands of the different double stranded transcription factor probes in the library and contacting the isolated transcription factor probes with the array under conditions suitable for hybridization of the strands of the different double stranded transcription factor probes to the hybridization probes in the array; and

comparing the activated transcription factors present in the different test samples.

2. A method according to claim 1 wherein at least 1% of the probes in the library have recognition sequences greater than 35 base pairs in length.

3. A method according to claim 1 wherein at least 1% of the probes in the library have recognition sequences greater than 40 base pairs in length.

4. A method according to claim 1 wherein at least 1% of the probes in the library have recognition sequences greater than 45 base pairs in length.

5. A method according to claim 1 wherein at least 5% of the probes in the library have recognition sequences greater than 35 base pairs in length.

6. A method according to claim 1 wherein at least 5% of the probes in the library have recognition sequences greater than 40 base pairs in length.

7. A method according to claim 1 wherein at least 5% of the probes in the library have recognition sequences greater than 45 base pairs in length.

8. A method according to claim 1 wherein the library comprises probes having recognition sequences between 20 and 40 base pairs in length.

9. A method according to claim 1 wherein the library comprises probes having recognition sequences between 25 and 35 base pairs in length.

10. A method according to claim 1 wherein the library comprises at least 5 different DNA recognition sequences.

11. A method according to claim 1 wherein the library comprises at least 10 different DNA recognition sequences.

12. A method according to claim 1 wherein the library comprises at least 20 different DNA recognition sequences.

13. A method according to claim 1 wherein the library comprises at least 50 different DNA recognition sequences.

14. A method according to claim 1 wherein the library comprises DNA recognition sequences for at least 5 different types of cells.

15. A method according to claim 1 wherein the library comprises DNA recognition sequences for at least 10 different types of cells.

16. A method according to claim 1 wherein the library comprises DNA recognition sequences for malignant, benign, and normal cell types.

17. A method according to claim 1 wherein the binding regions of the transcription factor probes on the array comprise at least two copies of a compliment to a portion of a recognition sequence comprised on the transcription factor probe.